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**Amendment to the Claims**

Claims 1 - 48 (Canceled)

49. (Previously presented): An isolated nucleic acid molecule comprising the nucleic acid sequence of SEQ ID NO. 7.

50. (Currently Amended): An isolated nucleic acid molecule encoding a polypeptide having an amino acid sequence of SEQ ID NO. 8 or an amino acid sequence having at least ~~40%~~ 60% sequence identity to SEQ ID NO: 8, wherein said polypeptide has 2, 5-diketo-D-gluconic acid (2,5-DKG) permease activity.

51. (Previously presented): The isolated nucleic acid molecule of claim 50, wherein the nucleic acid molecule encodes a polypeptide having at least 80% sequence identity to SEQ ID NO: 8.

52. (Previously presented): The isolated nucleic acid molecule of claim 50, wherein the nucleic acid molecule; encodes a polypeptide having at least 95% sequence identity to SEQ ID NO: 8.

53. (Previously presented): The isolate nucleic acid molecule of claim 50, wherein the nucleic acid molecule encodes the polypeptide of SEQ ID NO: 8.

54. (Previously presented): An isolated nucleic acid molecule comprising a nucleotide sequence having at least 40% sequence identity to SEQ ID NO: 7, wherein said nucleotide sequence encodes a polypeptide having 2,5-diketo-D-gluconic acid (2,5-DKG) permease activity.

55. (Previously presented): The isolated nucleic acid molecule of claim 54, wherein the nucleotide sequence has at least 80% sequence identity to SEQ ID NO: 7.

56. (Previously presented): The isolated nucleic acid molecule of claim 50 further comprising a promoter operably linked thereto.

57. (Previously presented): The isolated nucleic acid molecule of claim 56, wherein said promoter is a *lac* promoter.

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58. (Previously presented): A vector comprising the nucleic acid molecule of claim 50.
59. (Previously presented): The vector of claim 58 further comprising a spectinomycin resistance gene.
60. (Previously presented): A bacterial host comprising the vector of claim 58.
61. (Previously presented): A bacterial host comprising the nucleic acid molecule of claim 50.
62. (Previously presented): The bacteria host of claim 61, wherein said host lacks endogenous 2, 5-DKG permease activity.
63. (Previously presented): The bacterial host of claim 61, wherein the bacterial host is from the genus *Klebsiella*.
64. (Previously presented): The bacteria host of claim 63, wherein the *Klebsiella* is *Klebsiella oxytoca*.
65. (Previously presented): The bacterial host of claim 61, wherein the bacterial host is from the genus *Pantoea*.
66. (Previously presented): The bacterial host of claim 65, wherein the bacterial host is *Pantoea citrea*.
67. (Previously presented): The bacterial host of claim 61 further comprising a polynucleotide encoding a polypeptide having 2-keto reductase activity, said polypeptide having at least 80% amino acid sequence identity to SEQ ID NO: 14.
68. (Previously presented): The bacterial host of claim 61 further comprising a polynucleotide encoding a polypeptide having 5-keto reductase activity, said polypeptide having at least 80% amino acid sequence identity to SEQ ID NO: 16.

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69. (Currently amended): An isolated oligonucleotide comprising at least 20 contiguous nucleotides of the nucleotide sequence of SEQ ID NO: 7, wherein said oligonucleotide is used as a probe and hybridizes under stringent hybridization conditions to a nucleic acid that encodes a polypeptide having 2,5-diketo-D-gluconic acid (2,5-DKG) permease activity.

70. (Previously presented): The isolated oligonucleotide of claim 69 comprising at least 50 contiguous nucleotides of the nucleotide sequence of SEQ ID NO: 7

71. (Currently amended): A method of enhancing the production of 2-keto-L-gulonic acid (2-KLG) in a bacterial host comprising

a) transforming a bacterial host with a nucleic acid which encodes a first polypeptide having 2,5-diketo-D-gluconic acid (2, 5- DKG) permease activity, said first polypeptide having at least ~~40%~~ 60% amino acid sequence identity to SEQ ID NO: 8, wherein the bacterial host is capable of expressing an enzyme that catalyzes the conversion of 2, 5-DKG to 2-KLG,

b) culturing the transformed bacterial host under suitable culture conditions, and

c) obtaining 2-KLG.

72. (Previously presented): The method according to claim 71, wherein the amino acid sequence of the first polypeptide having 2,5-DKG permease activity has at least 80% amino acid sequence identity to SEQ ID NO: 8

73. (Previously presented): The method according to claim 71, wherein the first polypeptide having 2,5-DKG permease activity has the amino acid sequence of SEQ ID NO: 8.

74. (Previously presented): The method according to claim 71, wherein the bacterial host is from the genus *Pantoea*.

75. (Previously presented): The method according to claim 71, wherein the bacterial host is *E. coli*.

76. (Previously presented): A bacterial host obtained according to the method of claim 71.

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77. (Previously presented): The method according to claim 71 further comprising transforming the bacterial host with a polynucleotide encoding a second polypeptide, said second polypeptide having at least 80% amino acid sequence identity to SEQ ID NO: 10, wherein said second polypeptide has 2,5-DKG permease activity.
78. (Previously presented): The method according to claim 77, wherein the second polypeptide has at least 95% amino acid sequence identity to SEQ ID NO: 10.
79. (Previously presented): A bacterial host obtained according to the method of claim 77.
80. (Previously presented): The method according to claim 71 further comprising isolating the 2-KLG.
81. (Previously presented): The method according to claim 80 further comprising converting the 2-KLG to ascorbic acid.
82. (Previously presented): The method according to claim 71, wherein the bacterial host further includes a non-functional *tkrA* gene.
83. (New): The isolated nucleic acid molecule of claim 50, wherein the nucleic acid molecule encodes a polypeptide having at least 70% sequence identity to SEQ ID NO: 8.
84. (New): The method according to claim 71, wherein the amino acid sequence of the first polypeptide having 2,5-DKG permease activity has at least 70% amino acid sequence identity to SEQ ID NO: 8

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